SEQUENCE LISTING

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<110> ZOOROB, RIMA
   AUFFRAY, CHARLES
   CHAUSSE, ANNE-MARIE
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<120> REAGENTS AND METHODS FOR DETECTING GENES RELATED TO MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH AS CHICKEN

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<141> 2000-07-24

<150> PCT/FR98/02501

<151> 1998-11-23

<150> FR 97/14669

<151> 1997-11-21

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<170> PatentIn Ver. 2.1

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| tcagagtccc agggggaggt gtcccctggt gacctcatgg catcctcag ttc tca Phe Ser 215 | 1732 |
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| gtecetgtgt ecceaegtet aaccetetgt gacceetgee acatecetgt gteaecteet | 2055 |
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| gtc ctg ctc gac tac ttc ccc aca ctg atg aag gct gtg ggc tct tcg Val Leu Leu Asp Tyr Phe Pro Thr Leu Met Lys Ala Val Gly Ser Ser 260 265 270 | 2221 |
| gaa aaa atc ttt gag ttc ctg gac cgg gag cca cag gtc tca ccc tca Glu Lys Ile Phe Glu Phe Leu Asp Arg Glu Pro Gln Val Ser Pro Ser 275 280 285 | 2269 |
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| tgagggcgcg gggacatggc acatggtggg tttgtggcac tgggacatga tgagtgacac | 2599 |
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| att gcc cgt gca ctg ctg cgg gac ccc cgc atc ctc ata ctc gac gag Ile Ala Arg Ala Leu Leu Arg Asp Pro Arg Ile Leu Ile Leu Asp Glu 450 455 460 | 3439 |
| cac acc agc gcc ctg gac aat gag agc cag cag cag g tgggatgtcc His Thr Ser Ala Leu Asp Asn Glu Ser Gln Gln 465 470 475 | 3486 |
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| ctggcagtgg ctgaggaaca tccccctgaa ccgtttctcc tcccacagg tg gag 3660 cag gag atc ctc gca gcc aaa ggg tcg ggg cgt gca gtg ctg atg gtg 3708 Gln Glu Ile Leu Ala Ala Lys Gly Ser Gly Arg Ala Val Leu Met Val 480 acg ggg cgg gca gcc ctg gcg gcg cgg gca caa caa cga gtg gtg gtg ttg Thr Gly Arg Ala Ala Leu Ala Ala Arg Ala Gln Arg Val Val Val Leu 495 soo 505 gag ggg gga gag gtg cgg cag gag gga ccc ccc cac gag gtg gtg cgc Glu Gly Gly Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg Sio 525 ccc gtc agc ctt ntt gcg gga ctg ggg aca aca agg gag cac cgg ggg Pro Val Ser Leu Xaa Ala Gly Leu Gly Thr Thr Arg Glu His Arg Gly Sio 530 agg ggg aca gag gga tagcgggagt tttggatggg gagggcaggg ggtgggtggg Arg Gly Thr Glu Gly S45 atgtgggatg gggacactgc gcgttgggga cactgagggt ggaggtggg acaccggggc agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgagcc gggcgctg 4027 cggtaccgct gctgtacgac acacaacagc cacagcatgg atgcgagtgc gggggggggg | ggtccccatg gtcccctgtt ctggtgtccc cttatctcca ctcctggtgt ccctcggtcc | 3606 |
|---|---|------|
| Gin Giu Tile Leu Ala Ala Lys Gly Ser Gly Arg Ala Val Leu Met Val 480 acg ggg cgg gca gcc ctg gcg gcg cgg gca caa cga gtg gtg gtg ttg Thr Gly Arg Ala Ala Leu Ala Ala Arg Ala Gln Arg Val Val Val Leu 500 gag ggg gga gag gtg cgg cag gag gga ccc ccc cac gag gtg gtg cgc Glu Gly Gly Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg Sio 525 ccc gtc agc ctt ntt gcg gga ctg ggg aca aca agg gag cac cgg ggg Pro Val Ser Leu Xaa Ala Gly Leu Gly Thr Thr Arg Glu His Arg Gly 530 agg ggg gad aca gag gga tagcgggagt tttggatggg gagggcaggg ggtgggtggg 3907 Arg Gly Thr Glu Gly 545 atgtgggatg gggacactge gcgttgggga cactgagggt ggaggtgggg acaccggggc 3967 agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgagcc gggcgcgctg 4027 cggtaccgct gctgtacgac acacaaacggc cacagcatgg actgcagtgc cactgagtgc 4087 caccagggcc gggggtggga cacagaactg ggaataaagc cgcatgtttg t 4138 <210 > 8 <211 > 3133 <212 > DNA <220 > 222 > (273589, 787898, 9691175, 14631660, 17361864, 19632325, 23952553, 26222759, 28353011) <220 > 221 > modified_base 222 > (1)(3133) | | 3660 |
| Thr Gly Arg Ala Ala Leu Ala Ala Arg Ala Gln Arg Val Val Leu 495 gag ggg gga gag gtg cgg cag gag gga ccc ccc cac gag gtg gtg cgc Glu Gly Gly Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg 510 ccc gtc agc ctt ntt gcg gga ctg ggg aca aca agg gag cac cgg ggg Pro Val Ser Leu Xaa Ala Gly Leu Gly Thr Thr Arg Glu His Arg Gly 535 agg ggg aca gag gga tagcgggagt tttggatggg gagggcaggg ggtgggtggg 3907 Arg Gly Thr Glu Gly 545 atgtgggatg gggacactge gcgttgggga cactgagggt ggaggtgggg acaccggggg 3967 agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgaggc ggggggggg 3967 agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgagcc gggcgcgctg 4027 cggtaccgct gctgtacgac acacaacagc cacaagcatgg actgcagtgc cactgagtgc caccagggcc gggggtggga cacaagaactg ggaataaagc cgcatgtttg t 4138 <210 > 8 <211 > 3133 <212 > DNA <220 > <220 > <221 > ccc modified base <222 > (1) (3133) | Gln Glu Ile Leu Ala Ala Lys Gly Ser Gly Arg Ala Val Leu Met Val | 3708 |
| Glu Gly Gly Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg 510 525 525 525 525 525 525 525 525 525 52 | Thr Gly Arg Ala Ala Leu Ala Ala Arg Ala Gln Arg Val Val Leu | 3756 |
| Pro Val Ser Leu Xaa Ala Gly Leu Gly Thr Thr Arg Glu His Arg Gly 530 535 540 agg ggg aca gag gga tagcgggagt tttggatggg gagggcaggg ggtgggtggg 3907 Arg Gly Thr Glu Gly 545 atgtgggatg gggacactgc gcgttgggga cactgagggt ggaggtgggg acaccggggc 3967 agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgagcc gggcgcgctg 4027 cggtaccgct gctgtacgac acacaacggc cacagcatgg actgcagtgc cactgagtgc 4087 caccagggcc gggggtggga cacagaactg ggaataaagc cgcatgttg t 4138 <210 > 8 <211 > 3133 <212 > DNA <213 > Gallus sp. <220 > <221 > CDS <222 > (273589 , 787898 , 9691175 , 14631660 , 17361864 , 19632325 , 23952553 , 26222759 , 28353011) <220 > <221 > modified_base <222 > (1) (3133) | Glu Gly Gly Glu Val Arg Gln Glu Gly Pro Pro His Glu Val Val Arg | 3804 |
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| cggtaccgct gctgtacgac acacaacggc cacagcatgg actgeagtgc cactgagtgc 4087 caccagggcc gggggtggga cacagaactg ggaataaagc cgcatgtttg t 4138 <210 > 8 <211 > 3133 <212 > DNA <213 > Gallus sp. <220 > <221 > CDS <222 > (273589, 787898, 9691175, 14631660, 17361864, 19632325, 23952553, 26222759, 28353011) <220 > <221 > modified_base <222 > (1) (3133) | atgtgggatg gggacactgc gcgttgggga cactgagggt ggaggtgggg acaccggggc | 3967 |
| <pre>caccagggcc gggggtggga cacagaactg ggaataaagc cgcatgtttg t 4138 <210 > 8 <211 > 3133 <212 > DNA <213 > Gallus sp. <220 > <221 > CDS <222 > (273589, 787898, 9691175, 14631660, 17361864, 19632325, 23952553, 26222759, 28353011) <220 > <221 > modified_base <222 > (1)(3133)</pre> | agcaacaagg gaccacaaga gctgtgccgt gggcacatgg atgccgagcc gggcgcgctg | 4027 |
| <pre><210> 8 <211> 3133 <212> DNA <213> Gallus sp. <220> <221> CDS <222> (273589, 787898, 9691175, 14631660, 17361864,</pre> | cggtaccgct gctgtacgac acacaacggc cacagcatgg actgcagtgc cactgagtgc | 4087 |
| <pre><211> 3133 <212> DNA <213> Gallus sp. <220> <221> CDS <222> (273589, 787898, 9691175, 14631660, 17361864,</pre> | caccagggcc gggggtggga cacagaactg ggaataaagc cgcatgtttg t | 4138 |
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| 12237 It represents a, c, c, g, seller or unalown | <221> modified_base | |
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| gggctgcgcc tcctggtgct gggggggcc gggcagctgc tggcccccag gggaccccgt 180 | | |
| ggggctgcag tgctgctage atgggccccg ccatcttcct gaccctacgg ggctatgtag 240 | | 240 |

| gtctgcctgg agctcccccg gtgctgctgg cc atg gca acg ccg tcc tgg ctg Met Ala Thr Pro Ser Trp Leu 1 5 | 293 |
|---|-------------|
| gtg ctg acc cac ggg aca gct gtg gtg gca ttg ctc acc tgg agc ctc Val Leu Thr His Gly Thr Ala Val Val Ala Leu Leu Thr Trp Ser Leu 10 15 20 | 341 |
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| ggc tgt gcc ttc ctc ttc ctc gca ttg gct gca ctg ggt gag acc tca Gly Cys Ala Phe Leu Phe Leu Ala Leu Ala Ala Leu Gly Glu Thr Ser 60 65 70 | 485 |
| ttg ccc tac tgc acc ggg agg gct gtg gat gtc ctc cgc cag ggg gac Leu Pro Tyr Cys Thr Gly Arg Ala Val Asp Val Leu Arg Gln Gly Asp 75 80 85 | 533 |
| ggc ctc gcc gcc ttc acc gct gct gtc ggc ctc atg tgc ctg gcc tct Gly Leu Ala Ala Phe Thr Ala Ala Val Gly Leu Met Cys Leu Ala Ser 90 95 100 | 581 |
| gcc agc ag gtagggaccc cacatccctc cacaaaaccc catccacctc Ala Ser Ser 105 | 629 |
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| tcc agc ctg gtg tac cgg gac ctc gcc ttc ttc cag aac acc aca gca Ser Ser Leu Val Tyr Arg Asp Leu Ala Phe Phe Gln Asn Thr Thr Ala 130 135 140 | 898 |
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| ggtacagact gggggcactt ttgtccctgt ccccacacca tacccccagc tcaccgtact | 958 |
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| ggg cag gtg ctg ggg ctc tgc gcc ttc atg ctg ggg ctg tcc ccg cgc Gly Gln Val Leu Gly Leu Cys Ala Phe Met Leu Gly Leu Ser Pro Arg 175 180 185 | 1103 |
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| ctg aca atg ctg gca ctg ctc gaa gtg ccg ctc gcc gtc acc gca cgg Leu Thr Met Leu Ala Leu Leu Glu Val Pro Leu Ala Val Thr Ala Arg 190 195 200 | 1151 |
| aaa gtc tat gac acc cgg cac cag gtgatagcag ggatgggatg | 1205 |
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| ttctgggtgg gatcgggaca tccccgctga gccccatccc cacag gtg ctg cag Val Leu Gln 280 | 1744 |
| ttg gct gtg cag gca ctg gtg cta tac tgt ggg cac cag cag ctc cgc Leu Ala Val Gln Ala Leu Val Leu Tyr Cys Gly His Gln Gln Leu Arg 285 290 295 | 1792 |
| gaa ggg acc ctc act gcc ggc agc ctc gtc gcc ttc atc ctc tac cag Glu Gly Thr Leu Thr Ala Gly Ser Leu Val Ala Phe Ile Leu Tyr Gln 300 305 310 | 1840 |
| act aaa gct ggc agc tgc gtg cag gatccccatg actgtggcca catccccgtg Thr Lys Ala Gly Ser Cys Val Gln 315 320 | 1894 |
| tecceaceet gggtgetgtg ectgggggte acateceeat gtecetatee tgggtgetgt | 1954 |

| gcatgcag gca ctg gcg tac tcc tat ggt gac ctt ctg agc aat gca gtg Ala Leu Ala Tyr Ser Tyr Gly Asp Leu Leu Ser Asn Ala Val 325 330 335 | 2004 |
|---|------|
| gcc gcc tgc aag gtc ttt gat tac ctg gac tgg gag cga cct gtg ggt Ala Ala Cys Lys Val Phe Asp Tyr Leu Asp Trp Glu Arg Pro Val Gly 340 345 350 | 2052 |
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| caa gat gtc acc ttc gag ctg cgc ccc agt gag gtg acg gcg ttg gcg Gln Asp Val Thr Phe Glu Leu Arg Pro Ser Glu Val Thr Ala Leu Ala 385 390 395 | 2196 |
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| att gcc tac ggg atg gag gac tgc gaa gag gag gag atc ata gca gct Ile Ala Tyr Gly Met Glu Asp Cys Glu Glu Glu Glu Ile Ile Ala Ala 465 470 475 | 2496 |
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|--|---|
| cgg cgt ccc acc atc ctt atc ctc gac gaa g Arg Arg Pro Thr Ile Leu Ile Leu Asp Glu A 520 525 | cc acc agt gct ctg gat 2741 la Thr Ser Ala Leu Asp 30 535 |
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| cca cgg atg ctg gag aag gca gac cgc att g Pro Arg Met Leu Glu Lys Ala Asp Arg Ile V 565 570 | tg gtg ctg gag cat ggc 2939 Tal Val Leu Glu His Gly 575 |
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| ccc tac agc cgg ctg tta cag cac tgagaacca Pro Tyr Ser Arg Leu Leu Gln His 595 600 | t ggagcagctg gagtggcatg 3041 |
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Phe Ala Asn Glu Asp Gly Ala Ala Ala His Tyr Arg Gln Arg Leu Gln 180 185 190

Gln Ser His Arg Leu Glu Lys Lys Asp Val Ala Leu Tyr Thr Ala Ser 195 200 205

Leu Trp Thr Ser Gly Phe Ser Ala Leu Ala Leu Lys Met Gly Ile Leu 210 215 220

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Asp Val Leu Arg Gln Gly Asp Gly Leu Ala Ala Phe Thr Ala Ala Val 85 90 95

Gly Leu Met Cys Leu Ala Ser Ala Ser Ser Ser Leu Phe Ala Gly Cys 100 105 110

Arg Gly Leu Arg Phe Val Leu Arg Thr Arg Asp Gln Leu Phe Ser 115 120 125

Ser Leu Val Tyr Arg Asp Leu Ala Phe Phe Gln Asn Thr Thr Ala Ala 130 135 140

Glu Leu Ala Ser Arg Leu Thr Thr Asp Val Thr Leu Ala Ser Asn Val 145 150 155 160

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Thr Arg His Glr Met Leu Gln Arg Ala Val Leu Asp Ala Ala Asp 210 215 220

Thr Gly Ala Ala Val Gln Glu Ser Ile Ser Ser Ile Glu Met Val Arg 225 230 235 240

Val Phe Asn Gly Glu Glu Glu Glu His Arg Tyr Ser Gln Val Leu 245 250 255

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- Asp Tyr Glu His Arg Tyr Leu His Arg Gln Val Ala Leu Val Gly Gln 435 440 445
- Glu Pro Val Leu Phe Ser Gly Ser Ile Arg Asp Asn Ile Ala Tyr Gly
 450 455 460
- Met Glu Asp Cys Glu Glu Glu Glu Ile Ile Ala Ala Arg Ala Ala 465 470 475 480
- Gly Ala Leu Gly Phe Ile Ser Ala Leu Glu Gln Gly Phe Gly Thr Asp 485 490 495
- Val Gly Glu Arg Gly Gln Leu Ser Ala Gly Gln Lys Gln Arg Ile 500 505 510
- Ala Ile Ala Arg Ala Leu Val Arg Arg Pro Thr Ile Leu Ile Leu Asp 515 520 525
- Glu Ala Thr Ser Ala Leu Asp Gly Asp Ser Asp Ala Met Leu Gln Gln 530 540
- Trp Val Arg Asn Gly Gly Asp Arg Thr Val Leu Phe Ile Thr His Gln 545 550 555
- Pro Arg Met Leu Glu Lys Ala Asp Arg Ile Val Val Leu Glu His Gly 565 570 575
- Thr Val Ala Glu Met Gly Thr Pro Ala Glu Leu Arg Thr Arg Gly Gly 580 585 590

Pro Tyr Ser Arg Leu Leu Gln His

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